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# HLA-G transcription studies during the different stages of normal and malignant hematopoiesis.

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Specific expression of the non classical class I HLA-G gene on trophoblasts, the only fetal tissue in contact with maternal cells which lack MHC class I antigens, may indicate a role of this gene in fetal-maternal tolerance. We recently reported HLA-G transcription in peripheral blood leukocytes. In this work, we have investigated HLA-G transcription in hematopoietic stem cells, in different hematopoietic lineages and in malignant cells by using a RT-PCR technique. PCR amplification with primers specific to the exon 2 and the 3' untranslated region has enabled to detect HLA-G transcription in B and T cell populations. No transcription was found in CD34+ cells, in thymocytes, in polynuclear cells, in monocytes and in natural killer cells. Among the malignancies analyzed, HLA-G is transcribed in 2 of 13 cases of acute leukemia characterized by a monocytic contingent, in 3 of 6 CLL and in all the cases of B-NHL (n = 6). No HLA-G transcription was detected in myeloma (n = 2). The splicing type does not seem to be linked to a lymphocyte subpopulation nor to a malignant proliferation stage. These results suggest that HLA-G is a marker of mature lymphoid cells and may play an immunological function as a peptide presenting molecule. HLA-G transcription in some cases of malignancy might indicate a contribution to the tumoral progression by blocking natural killing reaction.

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